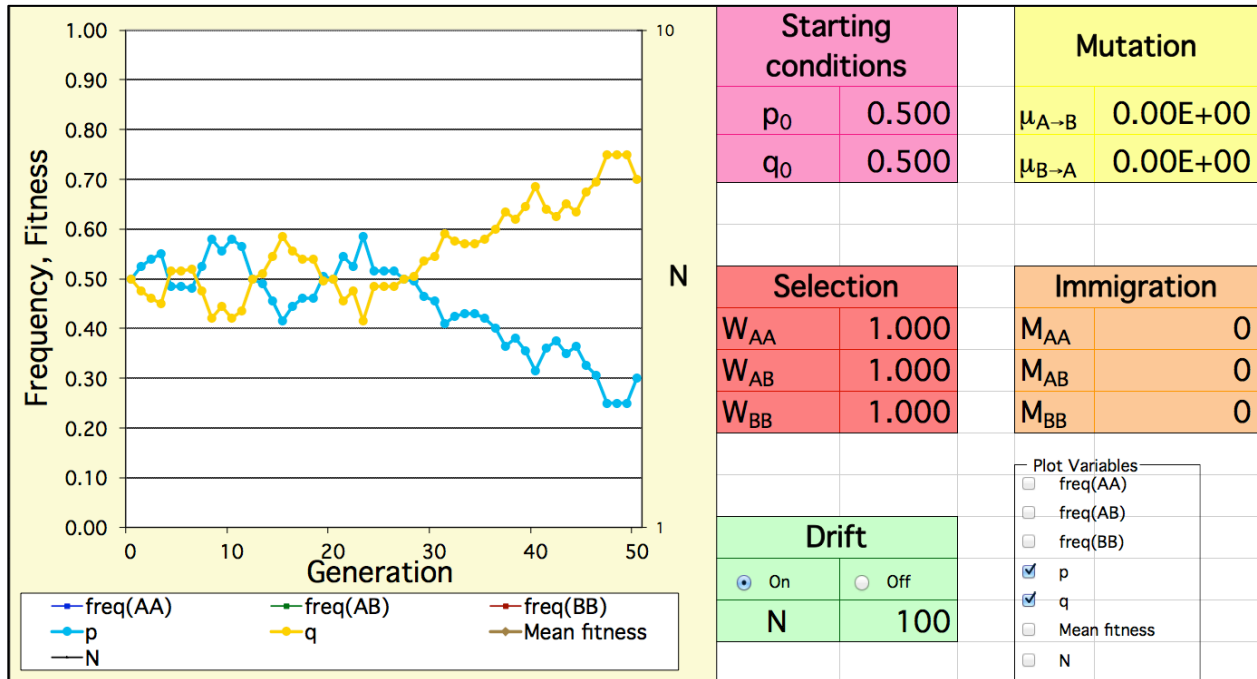


## ***DEME HELPFUL HINTS***



### Initial Settings for Deme Spreadsheet

- Starting Conditions:  $p_0 = 0.500$  and  $q_0 = 0.500$
- Mutation: 0.00E+00 in both cells
- Selection: 1.000 for all three cells
- Immigration: 0 for all three cells
- Drift: set button to “off” and  $N = 100$
- Plot Variables: check only p and q (all other options not checked)

## Variable 1 - Genetic Drift (Drift)

In nature, the process of **genetic drift** is defined as the change in the frequency of a gene variant (allele) in a population due to random sampling. While genetic drift is always occurring in nature, it may have different degrees of influence. This simulation allows for genetic drift to be turned “off” so that variables may be studied one at a time in this simulation. Keep in mind that in nature, genetic drift can never be turned “off”.

- With the initial settings in place, what happens when Drift is turned from “off” to “on”?
- With Drift turned “on”, press “control =” to do a second trial of simulation under the same conditions. Do the graphs show that allele frequencies ( $p$  and  $q$ ) remain the constant over 50 generations between the first and second trials? Press “control =” several more times and note what happens each time a new trial is run. Based on the results of multiple trials, is genetic drift a random or predictable process?
- With Drift turned “on”, change the population size exponentially ( $10 \rightarrow 100 \rightarrow 1000 \rightarrow 10,000 \rightarrow 100,000 \rightarrow 1,000,000$ ) and determine the influence of genetic drift on allele frequencies as population size increases. In doing so, use “control =” to run several trials at each population size. As well, determine the relationship between population size and gene fixation (loss of an allele in the population as indicated when Frequency = 0) due to random genetic drift?

## Variable 2 - Allele Frequencies (Starting Conditions)

**Note:** *Before starting, reset to the initial settings specified on page 1.*

- Change  $p_0$  to 0.100 and note that  $q_0$  will automatically adjust so that  $p + q = 1.0$  (or 100%). Since genetic drift, selection, mutation, and immigration are all set at 0, the population is in **Hardy-Weinberg equilibrium**. Examine the graph and determine what happens to the allele frequencies over 50 generations when a population is in Hardy-Weinberg equilibrium. Make a drawing of the  $p$  and  $q$  curves you observed in your lab notebook.
- Increase  $p_0$  by intervals of 0.100 (0.100, 0.200, 0.300, 0.400...etc.) until  $p_0$  reaches 1.0 and note what happens to the allele frequencies ( $p$  and  $q$ ) over 50 generations using the graph.
- Reset the Plot Variables so that only the frequency of AA ( $p^2$ ), AB ( $2pq$ ), and BB ( $q^2$ ) are checked. Then, repeat the steps outlined in the first two bullets and note what happens to each of the genotype frequencies over 50 generations using the graph. As well, summarize the trend and summarize the relationship between allele frequency and distribution of different phenotypes in a population?

### Variable 3 - Natural Selection (Selection)

**Note:** Before starting, reset to the initial settings specified on page 1.

When a selection value is increased for a specific genotype in this simulation, it means that the amount of **selection for** the genotype increases (if  $W > 1$ , then survival increases). Conversely, when a selection value is decreased for a specific genotype in this simulation, it means that the genotype is being **selected against** (if  $W < 1$ , then survival decreases).

#### Selection Against Homozygous Dominant Individuals

- Change the settings so that  $W_{AA} = 0.900$  and note what occurs to the allele frequencies ( $p_0$  and  $q_0$ ) and genotype frequencies (AA, AB, and BB) by adjusting the plot variables. Then, summarize the effects of selection against homozygous dominant individuals in regard to both the allele frequencies and genotype frequencies. As well, explain why the frequency of the homozygous dominant individuals (AA) is zero, but the frequency of the dominant allele ( $p$ ) is not zero by the time 50 generations have passed.
- Make sure Drift is turned “off” and exponentially increase the population size starting at  $N = 10$ . Note how this affects the effect of selection against the dominant allele over 50 generations. Are the effects of selection different in small populations vs. large populations when genetic drift is not a factor? Make a drawing of the  $p$  and  $q$  curves in your lab notebook.
- Turn Drift “on” and exponentially increase the population size starting at  $N = 10$  and note how this affects the effect of selection against the dominant allele over 50 generations. As well, run several trials at each population size using “Ctrl =”. Are the effects of selection more dramatic in a small or large population when genetic drift is a factor? Does population size influence the rate at which the homozygous dominant genotype is eventually lost within a population?

#### Selection Against Homozygous Recessive Individuals

- Return  $W_{AA}$  to 1.000 and make sure  $N=100$  and Drift is “off”. Then, change the Selection settings so that  $W_{BB} = 0.800$ . Note what occurs to the allele frequencies ( $p$  and  $q$ ) and genotype frequencies (AA, AB, and BB) by adjusting the plot variables. Then, summarize the effects of selection against homozygous recessive individuals in regard to both the allele frequencies and genotype frequencies.
- Make sure Drift is turned “off” and exponentially increase the population size starting at  $N = 10$ . Note how this affects the effect of selection against the recessive allele over 50 generations. Make a drawing of the  $p$  and  $q$  curves in your lab notebook.

- Turn Drift “on” and exponentially increase the population size starting at  $N = 10$  and note how this affects the effect of selection against the recessive allele over 50 generations. As well, run several trials at each population using “Ctrl =”. Does population size influence the rate at which the homozygous recessive genotype is eventually lost within a population?

### Selection Against Heterozygous Individuals

- Return  $W_{BB}$  to 1.000 and make sure  $N=100$  and Drift is “off”. Then, change the Selection settings so that  $W_{AB} = 0.800$ . Note what occurs to the allele frequencies ( $p$  and  $q$ ) and genotype frequencies (AA, AB, and BB) by adjusting the plot variables. Then, summarize the effects of selection against heterozygous individuals in regard to both the allele frequencies and genotype frequencies.
- Make sure Drift is turned “off” and exponentially increase the population size starting at  $N = 10$ . Note how this affects the frequency of the dominant and recessive alleles over 50 generations. Make a drawing of the  $p$  and  $q$  curves in your lab notebook. How does this drawing compare to the curves you drew for the selection against homozygous dominant and recessive individuals, respectively?
- Turn Drift “on” and exponentially increase the population size and note how this affects the effect of selection over 50 generations. As well, run several trials at each population using “Ctrl =”. Determine how selection against heterozygous individuals differs from selection against homozygous individuals and explain this phenomenon.

### Selection For the Dominant Allele

- Change the settings so that  $W_{AA} = 1.5$ ,  $W_{AB} = 1.0$ , and  $W_{BB} = 0.5$  and make sure  $N=100$  and Drift is “off”. Note what occurs to the allele frequencies ( $p$  and  $q$ ) and genotype frequencies (AA, AB, and BB) by adjusting the plot variables. Then, summarize the effects of selection for the dominant allele in regard to both the allele frequencies and genotype frequencies.
- Make sure Drift is turned “off” and exponentially increase the population size. Note how this affects the frequency of the dominant and recessive alleles over 50 generations. Make a drawing of the  $p$  and  $q$  curves in your lab notebook.
- Turn Drift “on” and exponentially increase the population size and note how this affects the effect of selection over 50 generations.

## Selection For the Recessive Allele

- Change the settings to that  $W_{AA}= 0.5$ ,  $W_{AB}=1$ , and  $W_{BB}= 1.5$  and make sure  $N=100$  and Drift is “off”. Note what occurs to the allele frequencies ( $p$  and  $q$ ) and genotype frequencies (AA, AB, and BB) by adjusting the plot variables. Then, summarize the effects of selection against the recessive allele in regard to both the allele frequencies and genotype frequencies.
- Make sure Drift is turned “off” and exponentially increase the population size. Note how this affects the frequency of the dominant and recessive alleles over 50 generations. Make a drawing of the  $p$  and  $q$  curves in your lab notebook. How does this drawing compare to the curves you drew for the selection for the dominant allele?
- Turn Drift “on” and exponentially increase the population size and note how this affects the effect of selection over 50 generations.

Hypothesize what will happen if the environment changes and the frequency of the newly defined fit allele is present at a low frequency? Will the fittest genotype remain in the population or will it be eliminated? Explain how this confirms or challenges the notion that natural selection means the survival of the fittest?

## Variable 4 - Mutation within a Gamete used in Fertilization (Mutation)

**Note:** Before starting, reset to the initial settings specified on page 1.

Factors such as mutagens that enter the environment via industrial waste can affect one allele more than another if a population is exposed to the mutagen. As a result, the mutation may have different affects on individuals with different phenotypes. In this simulation, the initial setting of 0.00E+00 indicates that no mutation is occurring. The E+00 is the exponent value and may be changed by typing in a number such as 0.1, 0.2, or 0.3 into the cell. The higher the value above 0.00E+00, the higher the mutation rate. As mutation occurs, the dominant allele ( $p$  or A) is mutated to the recessive allele ( $q$  or B), which serves to alter allele frequencies. As a result, it is not possible to introduce new alleles into the population using this simulation.

- **Differential Mutation Rates** - Increase the mutation rate of the dominant allele (A) in the upper cell by typing in 0.1. This will change the value in the cell to 1.00E-01 which is equal to  $1 \times 10^{-1}$  or 0.1. Note what happens to the frequency of the dominant and recessive alleles over 50 generations when the mutation rate of the dominant allele increases.
- **Equal Mutation Rates** - Increase the mutation rate of both the dominant and recessive alleles to 1.00E-01 and note what happens to the frequency of the dominant and recessive alleles over 50 generations.

## Variable 5 - Migration (Immigration)

**Note:** Before starting, reset to the initial settings specified on page 1.

Immigration is often a one time event that changes the allele frequency of a population. However, the Deme 1.0 program cannot simulate this type of change. When immigration values are changed in this simulation, the change occurs to each generation over the course of 50 generations shown in the graph. In other words, it shows continual immigration into an area. In this simulation, the symbol **M** refers to migration, and an increase in the value of  $M_{AA}$ ,  $M_{AB}$ , or  $M_{BB}$  will indicate the number of individuals that enter the population in each generation.

- **Immigration of Homozygous Dominant Individuals** - Change the setting of  $M_{AA}$  to 1 so that the population of 100 individuals has its gene pool changed by 1% in each generation. What is the affect on the frequency of the alleles (p and q) according to the graph?
- **Immigration of Homozygous Recessive Individuals** - Change the setting of  $M_{BB}$  to 1 so that the population of 100 individuals has its gene pool changed by 1% in each generation. What is the affect on the frequency of the alleles (p and q) according to the graph?
- **Immigration of Heterozygous Individuals** - Change the setting of  $M_{AB}$  to 1 so that the population of 100 individuals has its gene pool changed by 1% in each generation. What is the affect on the frequency of the alleles (p and q) according to the graph? Why does the immigration of heterozygous individuals have a different influence on the population than the immigration of homozygous individuals?